

ABSTRACT

The invention provides a method for reducing background in hybridization reactions of nucleic acids involving at least two homologous probes, wherein at least one of the probes is non-linear, or two homologous target sequences and a non-linear probe. Background is reduced by introducing an intended mismatch with a target sequence in at least one of the probes. The presence of the mismatch reduces the specificity of probes not entirely complementary to a target sequence to such an extent that the background signal is reduced. A set of mixed homologous probes, wherein at least one of the probes is non-linear, comprising such specific mismatch is also provided. The set can be used for the detection of variants of a family of nucleic acids, for instance a number of HIV variants. The invention also provides kits for carrying out the methods according to the invention.

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